



# INFLUENZA

## *science for the 21st Century*

***will include work in developing mathematical models to help predict the spread of influenza***

Since the 1918 pandemic that killed millions, influenza has continued as one of the world's most urgent public health problems. A highly contagious virus that constantly changes through mutation and genetic reassortment into new forms, allowing it to escape hosts' earlier-acquired immunity, influenza has proven difficult to treat.

Models developed by Los Alamos scientists will further understanding of the spread of influenza and other infectious diseases and help health researchers estimate and subsequently predict the impact of control measures on disease spread. Mathematical models for the spread of infectious diseases are essential tools for understanding the potential of an epidemic. Scientists can model sets of competing forces and study their interactions to gain understanding of the essential relationships among the social and biological mechanisms that influence the spread of a disease. This knowledge can help set priorities in research.

Influenza remains a disease of great concern, with the potential to kill large numbers of individuals. Various approaches to controlling influenza outbreaks have been tried, including vaccines and newly available drug treatments. Los Alamos is developing a model that will advance knowledge of the crucial, early phases of an epidemic.

There are two major components to the project. One component includes key biological parameters, such as immune system response, pathogen mutations, susceptibility and the ability of individuals to expose others to the infection. This component, which can be modified for other airborne organisms, will also incorporate the effect of an individual's recent vaccinations, recent illness or predisposition to a severe case.

The second component is Los Alamos' population mobility model called TRANSIMS, currently the definitive model for the transportation industry. Because advances in transportation technologies have made people, and the germs they carry with them, more mobile, interconnecting the biological and transportation components will give a fine-grained look at what happens in the early phases of an epidemic, allowing scientists to predict the spread of the disease within and between urban areas. The model will be a deployable tool, providing guidance to public health agencies on allocation of personnel, vaccines and other resources.

Two years ago, Los Alamos launched the Influenza Sequence Database. It acts as a repository for the many unpublished influenza viral sequences that reside in private databases at World Health Organization influenza surveillance centers worldwide. As with the Laboratory's other specialized databases, including the HIV, human papilloma virus and bacterial genomes databases, the Influenza Sequence Database is an efficient way to track evolutionary patterns. Because the influenza virus is constantly mutating, predicting its evolution will be critical in prevention efforts that use vaccines. Looking at the sequence progressions through time will help predict where the virus might go in the future.

Los Alamos' research efforts include developing statistical methods for detecting an "out-of-place" or unnatural virus. The rich collection of influenza sequences, with coordinated epidemiological information, provides a test bed for studying emerging viral diseases, whose increasing presence is a fact of life on a planet with changing patterns of urbanization.

**CONTACT:** Kay Roybal at [k\\_roybal@lanl.gov](mailto:k_roybal@lanl.gov) or (505) 665-0582. For more "Science for the 21st Century," go to <http://www.lanl.gov/orgs/pa/science21> on the World Wide Web.